



#10/c

SEQUENCE LISTING

<110> Huse, William D.
Wu, Herren

<120> Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
Acids Encoding Same and Methods of Use

<130> P-IX 3536

<140> US 09/339,922

<141> 1999-06-24

<160> 112

<170> PatentIn Ver. 2.1

<210> 1

<211> 351

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(351)

<220>

<223> Description of Artificial Sequence: grafted
antibody variable region

<400> 1

cag	gtg	cag	ctg	gtg	gag	tct	ggg	gga	ggc	gtt	gtg	cag	cct	gga	agg	48
Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	
1				5					10					15		
tcc	ctg	aga	ctc	tcc	tgt	gca	gcc	tct	gga	ttc	acc	ttc	agt	agc	tat	96
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr	
			20					25					30			
gac	atg	tct	tgg	gtt	cgc	cag	gct	ccg	ggc	aag	ggt	ctg	gag	tgg	gtc	144
Asp	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
		35					40					45				
gca	aaa	gtt	agt	agt	ggt	ggt	ggt	agc	acc	tac	tat	tta	gac	act	gtg	192
Ala	Lys	Val	Ser	Ser	Gly	Gly	Gly	Ser	Thr	Tyr	Tyr	Leu	Asp	Thr	Val	
	50					55					60					
cag	ggc	cga	ttc	acc	atc	tcc	aga	gac	aat	agt	aag	aac	acc	cta	tac	240
Gln	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	
	65				70				75					80		
ctg	caa	atg	aac	tct	ctg	aga	gcc	gag	gac	aca	gcc	gtg	tat	tac	tgt	288
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
			85					90					95			
gca	aga	cat	aac	tac	ggc	agt	ttt	gct	tac	tgg	ggc	caa	ggg	act	aca	336
Ala	Arg	His	Asn	Tyr	Gly	Ser	Phe	Ala	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	
			100					105					110			

113

c

gtg act gtt tct agt
Val Thr Val Ser Ser
115

351

<210> 2
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: grafted
antibody variable region

<400> 2
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30
Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val
50 55 60
Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Thr
100 105 110
Val Thr Val Ser Ser
115

<210> 3
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(321)
<220>
<223> Description of Artificial Sequence: grafted
antibody variable region

<400> 3
gag att gtg cta act cag tct cca gcc acc ctg tct ctc agc cca gga 48
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

gaa agg gcg act ctt tcc tgc cag gcc agc caa agt att agc aac cac 96
 Glu Arg Ala Thr Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
 20 25 30
 cta cac tgg tat caa caa agg cct ggt caa gcc cca agg ctt ctc atc 144
 Leu His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45
 aag tat cgt tcc cag tcc atc tct ggg atc ccc gcc agg ttc agt ggc 192
 Lys Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60
 agt gga tca ggg aca gat ttc acc ctc act atc tcc agt ctg gag cct 240
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
 65 70 75 80
 gaa gat ttt gca gtc tat tac tgt caa cag agt ggc agc tgg cct cac 288
 Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Gly Ser Trp Pro His
 85 90 95
 acg ttc gga ggg ggg acc aag gtg gaa att aag 321
 Thr Phe Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 4
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: grafted
 antibody variable region

<400> 4
 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 Glu Arg Ala Thr Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
 20 25 30
 Leu His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45
 Lys Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
 65 70 75 80
 Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Gly Ser Trp Pro His
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 5
 <211> 351
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(351)

<400> 5
 gaa gtg cag ctg gtg gag tct ggg gga ggc tta gtg aag cct gga agg 48
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Arg
 1 5 10 15
 tcc ctg aga ctc tcc tgt gca gcc tct gga ttc gct ttc agt agc tat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ser Tyr
 20 25 30
 gac atg tct tgg gtt cgc cag att ccg gag aag agg ctg gag tgg gtc 144
 Asp Met Ser Trp Val Arg Gln Ile Pro Glu Lys Arg Leu Glu Trp Val
 35 40 45
 gca aaa gtt agt agt ggt ggt ggt agc acc tac tat tta gac act gtg 192
 Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val
 50 55 60
 cag ggc cga ttc acc atc tcc aga gac aat gcc aag aac acc cta tac 240
 Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
 65 70 75 80
 ctg caa atg agc agt ctg aac tct gag gac aca gcc atg tat tac tgt 288
 Leu Gln Met Ser Ser Leu Asn Ser Glu Asp Thr Ala Met Tyr Tyr Cys
 85 90 95
 gca aga cat aac tac ggc agt ttt gct tac tgg ggc caa ggg act ctg 336
 Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Leu
 100 105 110
 gtc act gtc tct gca 351
 Val Thr Val Ser Ala
 115

<210> 6
 <211> 117
 <212> PRT
 <213> Mus musculus

<400> 6
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ser Tyr
 20 25 30
 Asp Met Ser Trp Val Arg Gln Ile Pro Glu Lys Arg Leu Glu Trp Val
 35 40 45

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d

Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val
50 55 60

Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Ser Ser Leu Asn Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ala
115

<210> 7
<211> 321
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(321)

<400> 7
gat att gtg cta act cag tct cca gcc acc ctg tct gtg aca cca gga 48
Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Thr Pro Gly
1 5 10 15

gat agc gtc agt ctt tcc tgc cag gcc agc caa agt att agc aac cac 96
Asp Ser Val Ser Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
20 25 30

cta cac tgg tat caa caa aaa tca cat gag tct cca agg ctt ctc atc 144
Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile
35 40 45

aag tat cgt tcc cag tcc atc tct ggg atc ccc tcc agg ttc agt ggc 192
Lys Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

agt gga tca ggg aca gat ttc gct ctc agt atc aac agt gtg gag act 240
Ser Gly Ser Gly Thr Asp Phe Ala Leu Ser Ile Asn Ser Val Glu Thr
65 70 75 80

gaa gat ttt gga atg tat ttc tgt caa cag agt ggc agc tgg cct cac 288
Glu Asp Phe Gly Met Tyr Phe Cys Gln Gln Ser Gly Ser Trp Pro His
85 90 95

acg ttc gga ggg ggg acc aag ctg gaa att aag 321
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 8
<211> 107

117

C

<212> PRT
<213> Mus musculus

<400> 8
Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Thr Pro Gly
1 5 10 15
Asp Ser Val Ser Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
20 25 30
Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile
35 40 45
Lys Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Ala Leu Ser Ile Asn Ser Val Glu Thr
65 70 75 80
Glu Asp Phe Gly Met Tyr Phe Cys Gln Gln Ser Gly Ser Trp Pro His
85 90 95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 9
<211> 84
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 9
caggtgcagc tgggtggagtc tgggggaggc gttgtgcagc ctggaaggct cctgagactc 60
tcctgtgcag cctctggatt cacc 84

<210> 10
<211> 84
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 10
aacttttgcg acccactcca gacccttgcc cggagcctgg cgaacccaag acatgtcata 60
gctactgaag gtgaatccag aggc 84

<210> 11
<211> 87
<212> DNA

118

2

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 11

tggtgcgcaa aagttagtag tggtggtggt agcacctact atttagacac tgtgcagggc 60
cgattcacca tctccagaga caatagt 87

<210> 12

<211> 81

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 12

tgcacagtaa tacacggctg tgcctcggc tctcagagag ttcatttgca ggtatagggc 60
gttcttacta ttgtctctgg a 81

<210> 13

<211> 75

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 13

gtgtattact gtgcaagaca taactacggc agttttgctt actggggcca agggactaca 60
gtgactgttt ctagt 75

<210> 14

<211> 87

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 14

gagattgtgc taactcagtc tccagccacc ctgtctctca gcccaggaga aagggcgact 60
ctttcctgcc aggccagcca aagtatt 87

<210> 15

<211> 72

<212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide

<400> 15
 gatgagaagc cttggggcct gaccaggcct ttgttgatac cagtgtaggt ggttgctaata 60
 actttggctg gc 72

<210> 16
 <211> 84
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide

<400> 16
 ccaaggcttc tcatawasta tcgttcccag tccatctctg ggatccccgc cagggttcagt 60
 ggcagtgat caggacaga tttc 84

<210> 17
 <211> 81
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide

<400> 17
 gctgccactc tgttgacagw aatagactgc aaaatcttca ggctccagac tggagatagt 60
 gaggtgaaa tctgtccctg a 81

<210> 18
 <211> 57
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide

<400> 18
 caacagagtgc gcagctggcc tcacacgttc ggagggggga ccaaggtgga aattaag 57

<210> 19
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide

120

Q

<400> 19
gcccaaccag ccatggccga tattgtgcta actcag 36

<210> 20
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 20
acagttggtg cagcatcagc 20

<210> 21
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 21
accctgtgg caaaagccga agtgcagctg gtggag 36

<210> 22
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 22
gatgggggtg tcgttttggc 20

<210> 23
<211> 87
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 23
gagattgtgc taactcagtc tccagccacc ctgtctctca gcccaggaga aagggcgact 60
ctttcctgcc aggcagcca aagtatt 87

<210> 24

<211> 75
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:
 oligonucleotide

 <400> 24
 ttagatgaga agccttgggg ctgaccagg cctttgttga taccagtga ggtggttgct 60
 aatactttgg ctggc 75

 <210> 25
 <211> 84
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:
 oligonucleotide

 <400> 25
 ccaaggcttc tcactaata tcgttcccag tccatctctg ggatccccgc caggttcagt 60
 ggcagtggat caggacaga tttc 84

 <210> 26
 <211> 81
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:
 oligonucleotide

 <400> 26
 gctgccactc tgttgacagt aatagactgc aaaatcttca ggctccagac tggagatagt 60
 gaggtgaaa tctgtccctg a 81

 <210> 27
 <211> 57
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:
 oligonucleotide

 <400> 27
 caacagagtg gcagctggcc tcacacgttc ggagggggga ccaaggtgga aattaag 57

 <210> 28
 <211> 10
 <212> PRT
 <213> Artificial Sequence

123

d

<220>
<223> Description of Artificial Sequence: antigen

<400> 28
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
1 5 10

<210> 29
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 29
gctactgaag gcgaatccag ag 22

<210> 30
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (11)..(13)
<223> NNN = codon specifying any amino acid other than
Lys.

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 30
gggaacgata nnngatgaga agc 23

<210> 31
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: grafted
antibody variable region

<220>
<221> variation
<222> (145)..(147)
<223> NNN=CGT OR ATG;

<400> 31
gagattgtgc taactcagtc tccagccacc ctgtctctca gcccaggaga aagggcgact 60
ctttcctgcc aggccagcca aagtattagc aaccacctac actggtatca acaaaggcct 120
ggccaagccc caaggcttct catcnnntat cgttcccagt ccattctctgg gatccccgcc 180

aggttcagtg gcagtggatc agggacagat ttcaccctca ctatctccag tctggagcct 240
 gaagattttg cagtctatta ctgtcaacag agtggcagct ggcctcacac gttcggaggg 300
 gggaccaagg tggaaattaa g 321

<210> 32
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> VARIANT
 <222> (49)
 <223> Xaa = Arg or Met

<220>
 <223> Description of Artificial Sequence: grafted
 antibody variable region

<400> 32
 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 Glu Arg Ala Thr Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
 20 25 30
 Leu His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45
 Xaa Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
 65 70 75 80
 Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Gly Ser Trp Pro His
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 33
 <211> 30
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(30)

<400> 33
 gga ttc acc ttc agt agc tat gac atg tct 30
 Gly Phe Thr Phe Ser Ser Tyr Asp Met Ser
 1 5 10

<210> 34

124

C

<211> 10
<212> PRT
<213> Mus musculus

<400> 34
Gly Phe Thr Phe Ser Ser Tyr Asp Met Ser
1 5 10

<210> 35
<211> 30
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(30)

<400> 35
tgg gtc gca aaa gtt agt agt ggt ggt ggt 30
Trp Val Ala Lys Val Ser Ser Gly Gly Gly
1 5 10

<210> 36
<211> 10
<212> PRT
<213> Mus musculus

<400> 36
Trp Val Ala Lys Val Ser Ser Gly Gly Gly
1 5 10

<210> 37
<211> 30
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(30)

<400> 37
agc acc tac tat tta gac act gtg cag ggc 30
Ser Thr Tyr Tyr Leu Asp Thr Val Gln Gly
1 5 10

<210> 38
<211> 10
<212> PRT
<213> Mus musculus

<400> 38
Ser Thr Tyr Tyr Leu Asp Thr Val Gln Gly

125

C

1

5

10

<210> 39
 <211> 30
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(30)

<400> 39
 gca aga cat aac tac ggc agt ttt gct tac
 Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr
 1 5 10

30

<210> 40
 <211> 10
 <212> PRT
 <213> Mus musculus

<400> 40
 Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr
 1 5 10

<210> 41
 <211> 39
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(39)

<400> 41
 cag gcc agc caa agt att agc aac cac cta cac tgg tat
 Gln Ala Ser Gln Ser Ile Ser Asn His Leu His Trp Tyr
 1 5 10

39

<210> 42
 <211> 13
 <212> PRT
 <213> Mus musculus

<400> 42
 Gln Ala Ser Gln Ser Ile Ser Asn His Leu His Trp Tyr
 1 5 10

<210> 43
 <211> 33

<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(33)

<400> 43
ctt ctc atc cgt tat cgt tcc cag tcc atc tct
Leu Leu Ile Arg Tyr Arg Ser Gln Ser Ile Ser
1 5 10

33

<210> 44
<211> 11
<212> PRT
<213> Mus musculus

<400> 44
Leu Leu Ile Arg Tyr Arg Ser Gln Ser Ile Ser
1 5 10

<210> 45
<211> 27
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(27)

<400> 45
caa cag agt ggc agc tgg cct cac acg
Gln Gln Ser Gly Ser Trp Pro His Thr
1 5

27

<210> 46
<211> 9
<212> PRT
<213> Mus musculus

<400> 46
Gln Gln Ser Gly Ser Trp Pro His Thr
1 5

<210> 47
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(30)

127

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<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 47
gga act acc ttc agt agc tat gac atg tct 30
Gly Thr Thr Phe Ser Ser Tyr Asp Met Ser
1 5 10

<210> 48
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 48
Gly Thr Thr Phe Ser Ser Tyr Asp Met Ser
1 5 10

<210> 49
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(30)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 49
gga ttc acc tgg agt agc tat gac atg tct 30
Gly Phe Thr Trp Ser Ser Tyr Asp Met Ser
1 5 10

<210> 50
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 50
Gly Phe Thr Trp Ser Ser Tyr Asp Met Ser
1 5 10

<210> 51
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(30)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 51
gga ttc acc ttc ctg agc tat gac atg tct 30
Gly Phe Thr Phe Leu Ser Tyr Asp Met Ser
1 5 10

<210> 52
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 52
Gly Phe Thr Phe Leu Ser Tyr Asp Met Ser
1 5 10

<210> 53
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(30)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 53
tgg gtc gca aaa gtt aaa agt ggt ggt ggt 30
Trp Val Ala Lys Val Lys Ser Gly Gly Gly
1 5 10

<210> 54
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 54
Trp Val Ala Lys Val Lys Ser Gly Gly Gly
1 5 10

<210> 55
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(30)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 55
agc acc tac tat cct gac act gtg cag ggc 30
Ser Thr Tyr Tyr Pro Asp Thr Val Gln Gly
1 5 10

<210> 56
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 56
Ser Thr Tyr Tyr Pro Asp Thr Val Gln Gly
1 5 10

<210> 57
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(30)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 57

agc acc tac tat tta gac act gtg gag ggc
Ser Thr Tyr Tyr Leu Asp Thr Val Glu Gly
1 5 10

30

<210> 58
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 58
Ser Thr Tyr Tyr Leu Asp Thr Val Glu Gly
1 5 10

<210> 59
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(30)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 59
gca aga cat aac cat ggc agt ttt gct tac
Ala Arg His Asn His Gly Ser Phe Ala Tyr
1 5 10

30

<210> 60
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 60
Ala Arg His Asn His Gly Ser Phe Ala Tyr
1 5 10

<210> 61
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(30)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 61
gca aga cat aac tac ggc agt tat gct tac
Ala Arg His Asn Tyr Gly Ser Tyr Ala Tyr
1 5 10

30

<210> 62
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 62
Ala Arg His Asn Tyr Gly Ser Tyr Ala Tyr
1 5 10

<210> 63
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(30)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 63
gca aga cat aac tac ggc agt ttt gat tac
Ala Arg His Asn Tyr Gly Ser Phe Asp Tyr
1 5 10

30

<210> 64
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 64

132

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Ala Arg His Asn Tyr Gly Ser Phe Asp Tyr
1 5 10

<210> 65
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(30)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 65
gca aga cat aac tac ggc agt ttt tat tac 30
Ala Arg His Asn Tyr Gly Ser Phe Tyr Tyr
1 5 10

<210> 66
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 66
Ala Arg His Asn Tyr Gly Ser Phe Tyr Tyr
1 5 10

<210> 67
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(30)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 67
gca aga cat aac tac ggc agt ttt gct tct 30
Ala Arg His Asn Tyr Gly Ser Phe Ala Ser
1 5 10

<210> 68
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 68

Ala Arg His Asn Tyr Gly Ser Phe Ala Ser
1 5 10

<210> 69
<211> 30
<212> DNA
<213> Artificial Sequence

<220>

<221> CDS
<222> (1)..(30)

<220>

<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 69

gca aga cat aac tac ggc agt ttt gct act 30
Ala Arg His Asn Tyr Gly Ser Phe Ala Thr
1 5 10

<210> 70
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 70

Ala Arg His Asn Tyr Gly Ser Phe Ala Thr
1 5 10

<210> 71
<211> 30
<212> DNA
<213> Artificial Sequence

<220>

<221> CDS
<222> (1)..(30)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 71
gca aga cat aac tac ggc agt ttt gct gat 30
Ala Arg His Asn Tyr Gly Ser Phe Ala Asp
1 5 10

<210> 72
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 72
Ala Arg His Asn Tyr Gly Ser Phe Ala Asp
1 5 10

<210> 73
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(30)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 73
gca aga cat aac tac ggc agt ttt gct gag 30
Ala Arg His Asn Tyr Gly Ser Phe Ala Glu
1 5 10

<210> 74
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 74
Ala Arg His Asn Tyr Gly Ser Phe Ala Glu
1 5 10

<210> 75
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(30)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 75
gca aga cat aac tac ggc agt ttt gct atg 30
Ala Arg His Asn Tyr Gly Ser Phe Ala Met
1 5 10

<210> 76
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 76
Ala Arg His Asn Tyr Gly Ser Phe Ala Met
1 5 10

<210> 77
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(30)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 77
gca aga cat aac tac ggc agt ttt gct ggg 30
Ala Arg His Asn Tyr Gly Ser Phe Ala Gly
1 5 10

<210> 78
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 78
Ala Arg His Asn Tyr Gly Ser Phe Ala Gly
1 5 10

<210> 79
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(30)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 79
gca aga cat aac tac ggc agt ttt gct gct 30
Ala Arg His Asn Tyr Gly Ser Phe Ala Ala
1 5 10

<210> 80
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 80
Ala Arg His Asn Tyr Gly Ser Phe Ala Ala
1 5 10

<210> 81
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(39)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 81

cag gcc agc caa agt att agc aac ttt cta cac tgg tat
Gln Ala Ser Gln Ser Ile Ser Asn Phe Leu His Trp Tyr
1 5 10

39

<210> 82
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 82
Gln Ala Ser Gln Ser Ile Ser Asn Phe Leu His Trp Tyr
1 5 10

<210> 83
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(33)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 83
ctt ctc atc cgt tat tct tcc cag tcc atc tct
Leu Leu Ile Arg Tyr Ser Ser Gln Ser Ile Ser
1 5 10

33

<210> 84
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 84
Leu Leu Ile Arg Tyr Ser Ser Gln Ser Ile Ser
1 5 10

<210> 85
<211> 27
<212> DNA
<213> Artificial Sequence

138

C

<220>
<221> CDS
<222> (1)..(27)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 85
caa cag agt aat agc tgg cct cac acg
Gln Gln Ser Asn Ser Trp Pro His Thr
1 5

27

<210> 86
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 86
Gln Gln Ser Asn Ser Trp Pro His Thr
1 5

<210> 87
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(27)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 87
caa cag agt act agc tgg cct cac act
Gln Gln Ser Thr Ser Trp Pro His Thr
1 5

27

<210> 88
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 88

Gln Gln Ser Thr Ser Trp Pro His Thr
1 5

<210> 89
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(27)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 89
caa cag agt ggc agc tgg cct ctg acg
Gln Gln Ser Gly Ser Trp Pro Leu Thr
1 5

27

<210> 90
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 90
Gln Gln Ser Gly Ser Trp Pro Leu Thr
1 5

<210> 91
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(27)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 91
caa cag agt ggc agc tgg cct cag acg
Gln Gln Ser Gly Ser Trp Pro Gln Thr
1 5

27

140

C

<210> 92
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 92
Gln Gln Ser Gly Ser Trp Pro Gln Thr
1 5

<210> 93
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(30)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 93
gca aga cat aac cat ggc agt ttt tat tct 30
Ala Arg His Asn His Gly Ser Phe Tyr Ser
1 5 10

<210> 94
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 94
Ala Arg His Asn His Gly Ser Phe Tyr Ser
1 5 10

<210> 95
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(30)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 95
gca aga cat aac cat ggc agt ttt gct tct 30
Ala Arg His Asn His Gly Ser Phe Ala Ser
1 5 10

<210> 96
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 96
Ala Arg His Asn His Gly Ser Phe Ala Ser
1 5 10

<210> 97
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(30)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 97
gca aga cat aac tac ggc agt ttt tat gag 30
Ala Arg His Asn Tyr Gly Ser Phe Tyr Glu
1 5 10

<210> 98
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 98
Ala Arg His Asn Tyr Gly Ser Phe Tyr Glu
1 5 10

142

C

<210> 99
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(30)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 99
gca aga cat aac tac ggc agt ttt tat tct 30
Ala Arg His Asn Tyr Gly Ser Phe Tyr Ser
1 5 10

<210> 100
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 100
Ala Arg His Asn Tyr Gly Ser Phe Tyr Ser
1 5 10

<210> 101
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(51)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 101
aaa gtt agt agt ggt ggt ggt agc acc tac tat tta gac act gtg cag 48
Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val Gln
1 5 10 15

ggc 51
Gly

<210> 102
<211> 17

143

C

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 102
Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val Gln
1 5 10 15

Gly

<210> 103
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(51)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 103
aaa gtt agt agt ggt ggt ggt agc acc tac tat cca gac act gtg cag 48
Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Pro Asp Thr Val Gln
1 5 10 15

ggc 51
Gly

<210> 104
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 104
Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Pro Asp Thr Val Gln
1 5 10 15

Gly

<210> 105
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(24)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 105
cat ctt cat ggc agt ttt gct tct
His Leu His Gly Ser Phe Ala Ser
1 5

24

<210> 106
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 106
His Leu His Gly Ser Phe Ala Ser
1 5

<210> 107
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(33)

<220>
<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 107
cag gcc agc caa agt att agc aac cac cta cac
Gln Ala Ser Gln Ser Ile Ser Asn His Leu His
1 5 10

33

<210> 108
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Mutated

145

C

complementarity determining region (CDR)

<400> 108

Gln Ala Ser Gln Ser Ile Ser Asn His Leu His
1 5 10

<210> 109

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(33)

<220>

<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 109

cag gcc agc caa agt att agc aac ttc cta cac
Gln Ala Ser Gln Ser Ile Ser Asn Phe Leu His
1 5 10

33

<210> 110

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 110

Gln Ala Ser Gln Ser Ile Ser Asn Phe Leu His
1 5 10

<210> 111

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(21)

<220>

<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 111

tat cgt tcc cag tcc atc tct
Tyr Arg Ser Gln Ser Ile Ser

21

146

C

1

5

<210> 112

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Mutated
complementarity determining region (CDR)

<400> 112

Tyr Arg Ser Gln Ser Ile Ser

1

5

147

C